

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-15.p2n.rng.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-15.p2n.rng.

[start](#)

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:32:04 ; Search time 332.409 Seconds
(without alignments)
1038.259 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKALKKLKKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102051_79/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561@CGN_1_1_1975@runat_11082006_102051_79 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*

2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
	1	80	47.3	750	12	ADG83792 Lamprey p
	2	76	45.0	718	12	ADG83794 Lamprey p
	3	75	44.4	790	12	ADG83788 Lamprey p
	4	69	40.8	676	12	ADG83790 Lamprey p
c	5	66	39.1	161334	11	ACN44334 Human gen
c	6	64.5	38.2	1730	2	AAQ44429 Kcal-1.8
c	7	64.5	38.2	1730	2	AAT61043 Porcine a
c	8	63.5	37.6	413	8	ABX36485 Bovine ES
	9	63.5	37.6	431	8	ABX39359 Bovine ES
	10	61	36.1	648	10	ABZ40693 N. gonorr
	11	61	36.1	132942	14	ADZ12611 Murine ca
c	12	60.5	35.8	1542	6	ABK35258 Human cDN
c	13	60.5	35.8	1549	10	ADI15977 Human PP
c	14	60.5	35.8	1549	12	ADJ81703 Tumour an
c	15	60.5	35.8	1668	14	AED18045 Fibrotic
c	16	60.5	35.8	1765	10	ADJ56437 Human cDN
c	17	60.5	35.8	2045	12	ADJ62780 Human cDN
c	18	60.5	35.8	2045	14	ADX07279 Cyclin-de
c	19	60.5	35.8	2138	11	ACN88839 Breast ca
	20	60	35.5	111	10	ABZ40692 N. gonorr
	21	60	35.5	742	5	AAS72405 DNA encod
	22	60	35.5	1644	6	ABK49105 Human cDN
	23	60	35.5	13608	4	AAK87529 Human imm
	24	60	35.5	20001	13	ADT77140 Type II d
c	25	60	35.5	21761	4	ABK42793 Genomic s
c	26	60	35.5	21761	4	AAK66660 Human imm
c	27	60	35.5	21761	9	ADB60949 Connectiv
	28	60	35.5	48275	3	AAA81501 N. mening
c	29	60	35.5	110000	3	AAA81489 N. mening
c	30	60	35.5	349980	3	AAF21610 Neisseria
	31	59.5	35.2	363	6	AAD25405 Human gon
	32	59.5	35.2	363	8	AAD53500 Human gon
	33	59.5	35.2	363	14	ADV43766 Human psy
	34	59.5	35.2	423	9	AAL62565 Human gon
	35	59.5	35.2	1142	12	ADJ40083 Plant cDN
c	36	59	34.9	186	13	ACF90925 Human SIR
	37	59	34.9	488	10	ADB50985 Primary r

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-15.p2n.rni.

[Score Home Page](#)
[Retrieve Application List](#)
[SCORE System Overview](#)
[SCORE FAQ](#)
[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10617561 and Search Result us-10-6: 561-15.p2n.rni.

[start](#)

[Go Back to previous p](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:51:34 ; Search time 104.299 Seconds
(without alignments)
888.020 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKLKKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102057_179/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10617561_CGN_1_1_529@runat_11082006_102057_179 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA: *
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq: *

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
No.						
1	80	47.3	750	3	US-10-170-096A-5	Sequence 5, Appli
2	76	45.0	718	3	US-10-170-096A-7	Sequence 7, Appli
3	75	44.4	790	3	US-10-170-096A-1	Sequence 1, Appli
4	69	40.8	676	3	US-10-170-096A-3	Sequence 3, Appli
c 5	64.5	38.2	1730	2	US-07-923-095-1	Sequence 1, Appli
c 6	64.5	38.2	1730	2	US-08-229-511-1	Sequence 1, Appli
c 7	64.5	38.2	1730	2	US-08-314-979-1	Sequence 1, Appli
c 8	64.5	38.2	1730	2	US-08-436-716-1	Sequence 1, Appli
c 9	60.5	35.8	1371	3	US-09-949-016-4550	Sequence 4550, Ap
10	58	34.3	1221	3	US-09-248-796A-4117	Sequence 4117, Ap
11	58	34.3	1635	3	US-09-722-377-12	Sequence 12, Appl
c 12	58	34.3	2244	3	US-09-489-039A-911	Sequence 911, App
13	58	34.3	88036	3	US-09-949-016-15335	Sequence 15335, A
14	57	33.7	300	2	US-08-668-255-6	Sequence 6, Appli
15	57	33.7	300	2	US-08-668-255-8	Sequence 8, Appli
16	57	33.7	360	2	US-08-668-255-4	Sequence 4, Appli
17	57	33.7	553	3	US-09-148-545-133	Sequence 133, App
18	57	33.7	553	3	US-09-621-011-133	Sequence 133, App
19	57	33.7	2029	3	US-10-104-047-874	Sequence 874, App
20	56.5	33.4	1487	3	US-09-722-971-3	Sequence 3, Appli
21	56.5	33.4	18705	5	US-09-984-429-463	Sequence 463, App
22	56.5	33.4	18715	5	US-09-984-429-387	Sequence 387, App
c 23	56.5	33.4	142504	3	US-09-949-016-13693	Sequence 13693, A
c 24	56.5	33.4	142506	3	US-09-949-016-12474	Sequence 12474, A
c 25	56	33.1	16720	3	US-09-902-540-1168	Sequence 1168, Ap
c 26	55	32.5	601	3	US-09-949-016-30307	Sequence 30307, A
c 27	55	32.5	601	3	US-09-949-016-196295	Sequence 196295,
28	55	32.5	963	3	US-09-902-540-3521	Sequence 3521, Ap
29	55	32.5	8590	3	US-09-949-016-5562	Sequence 5562, Ap
30	55	32.5	10300	3	US-09-949-016-636	Sequence 636, App
31	55	32.5	38575	3	US-09-949-016-17304	Sequence 17304, A
c 32	55	32.5	59319	3	US-09-949-016-16115	Sequence 16115, A
33	55	32.5	119153	3	US-09-949-016-12378	Sequence 12378, A
34	54.5	32.2	630	2	US-08-185-414E-1	Sequence 1, Appli
35	54.5	32.2	2890	3	US-08-848-810-1	Sequence 1, Appli
36	54.5	32.2	2940	2	US-08-428-415-3	Sequence 3, Appli
37	54.5	32.2	2940	2	US-08-379-685-3	Sequence 3, Appli
38	54.5	32.2	2940	2	US-08-854-029-3	Sequence 3, Appli
39	54.5	32.2	2940	3	US-08-428-762-3	Sequence 3, Appli
40	54.5	32.2	3118	4	US-09-880-107-3035	Sequence 3035, Ap
c 41	54.5	32.2	36820	3	US-09-949-016-16665	Sequence 16665, A
42	54.5	32.2	283538	3	US-09-949-016-13506	Sequence 13506, A

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-15.p2n.rnpbm.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-15.p2n.rnpbm.

[start](#)

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:58:24 ; Search time 1105.86 Seconds
(without alignments)
550.013 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKALKKLKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102100_235/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10617561_CGN_1_1_5513_runat_11082006_102100_235 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*


```

1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	80	47.3	750	7	US-10-170-096A-5	Sequence 5, Appli
	2	80	47.3	750	16	US-11-172-274-5	Sequence 5, Appli
	3	76	45.0	718	7	US-10-170-096A-7	Sequence 7, Appli
	4	76	45.0	718	16	US-11-172-274-7	Sequence 7, Appli
	5	75	44.4	790	7	US-10-170-096A-1	Sequence 1, Appli
	6	75	44.4	790	16	US-11-172-274-1	Sequence 1, Appli
	7	69	40.8	676	7	US-10-170-096A-3	Sequence 3, Appli
	8	69	40.8	676	16	US-11-172-274-3	Sequence 3, Appli
c	9	66	39.1	161334	6	US-10-087-192-730	Sequence 730, App
c	10	63.5	37.6	413	3	US-09-960-352-1650	Sequence 1650, Ap
	11	63.5	37.6	431	3	US-09-960-352-4524	Sequence 4524, Ap
c	12	63	37.3	586	9	US-10-425-115-95993	Sequence 95993, A
c	13	62	36.7	464	8	US-10-437-963-69292	Sequence 69292, A
	14	62	36.7	1491	8	US-10-335-977-4737	Sequence 4737, Ap
	15	62	36.7	1710	8	US-10-335-977-4738	Sequence 4738, Ap
	16	61	36.1	232	9	US-10-425-115-90482	Sequence 90482, A
	17	61	36.1	648	10	US-10-467-657-5975	Sequence 5975, Ap
c	18	61	36.1	651	9	US-10-425-115-110906	Sequence 110906,
c	19	60.5	35.8	658	10	US-10-956-157-3940	Sequence 3940, Ap
	20	60.5	35.8	658	10	US-10-956-157-9175	Sequence 9175, Ap
c	21	60.5	35.8	1400	10	US-10-956-157-6626	Sequence 6626, Ap
c	22	60.5	35.8	1542	3	US-09-822-849A-396	Sequence 396, App
c	23	60.5	35.8	1549	9	US-10-734-049A-321	Sequence 321, App
c	24	60.5	35.8	1765	6	US-10-084-817-243	Sequence 243, App
c	25	60.5	35.8	2045	8	US-10-439-703-50	Sequence 50, Appl
c	26	60.5	35.8	2045	10	US-10-956-157-1391	Sequence 1391, Ap
c	27	60.5	35.8	2138	6	US-10-198-846-9989	Sequence 9989, Ap
	28	60.5	35.8	160103	7	US-10-085-117-262	Sequence 262, App
	29	60	35.5	111	10	US-10-467-657-5973	Sequence 5973, Ap
c	30	60	35.5	578	9	US-10-425-115-136371	Sequence 136371,
	31	60	35.5	742	10	US-10-450-763-8209	Sequence 8209, Ap
c	32	60	35.5	21761	3	US-09-764-847-1680	Sequence 1680, Ap
c	33	60	35.5	21761	6	US-10-092-154-1680	Sequence 1680, Ap
c	34	60	35.5	45045	9	US-10-741-600-17689	Sequence 17689, A
	35	60	35.5	48275	10	US-10-915-740A-48	Sequence 48, Appl

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-15.p2n.rnpbn.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-15.p2n.rnpbn.

[start](#)

[Go Back to previous pag](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:59:05 ; Search time 134.891 Seconds
(without alignments)
582.767 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102102_304/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561_@CGN_1_1_661_@runat_11082006_102102_304 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	64	37.9	2468	8	US-11-266-748A-27808	Sequence 27808, A
	2	61	36.1	442	9	US-11-348-413-2009	Sequence 2009, Ap
	3	60.5	35.8	931	8	US-11-266-748A-113960	Sequence 113960,
c	4	60.5	35.8	931	8	US-11-266-748A-161648	Sequence 161648,
c	5	60.5	35.8	970	8	US-11-266-748A-191356	Sequence 191356,
c	6	60.5	35.8	970	8	US-11-266-748A-225772	Sequence 225772,
c	7	60.5	35.8	993	8	US-11-266-748A-168581	Sequence 168581,
c	8	60.5	35.8	1408	8	US-11-266-748A-183944	Sequence 183944,
c	9	60.5	35.8	1493	8	US-11-266-748A-168580	Sequence 168580,
c	10	60.5	35.8	1565	8	US-11-266-748A-19663	Sequence 19663, A
c	11	60.5	35.8	1795	8	US-11-266-748A-249880	Sequence 249880,
c	12	60.5	35.8	1795	8	US-11-266-748A-274644	Sequence 274644,
	13	60.5	35.8	1795	8	US-11-266-748A-310397	Sequence 310397,
c	14	60.5	35.8	2046	8	US-11-266-748A-73892	Sequence 73892, A
c	15	60.5	35.8	2046	8	US-11-266-748A-108070	Sequence 108070,
	16	60.5	35.8	2046	8	US-11-266-748A-126703	Sequence 126703,
c	17	60	35.5	546	8	US-11-266-748A-207482	Sequence 207482,
	18	60	35.5	550	8	US-11-266-748A-361880	Sequence 361880,
c	19	60	35.5	550	8	US-11-266-748A-445259	Sequence 445259,
	20	60	35.5	896	8	US-11-266-748A-117314	Sequence 117314,
c	21	60	35.5	896	8	US-11-266-748A-159478	Sequence 159478,
	22	60	35.5	2135	8	US-11-266-748A-185503	Sequence 185503,
	23	60	35.5	2135	8	US-11-266-748A-192966	Sequence 192966,
	24	59.5	35.2	423	8	US-11-266-748A-115612	Sequence 115612,
c	25	59.5	35.2	423	8	US-11-266-748A-157776	Sequence 157776,
	26	59.5	35.2	1901	9	US-11-218-305-20231	Sequence 20231, A
	27	59	34.9	1000	8	US-11-266-748A-393342	Sequence 393342,
c	28	59	34.9	1000	8	US-11-266-748A-464388	Sequence 464388,
c	29	59	34.9	1287	9	US-11-218-305-22060	Sequence 22060, A
	30	59	34.9	1414	8	US-11-266-748A-27774	Sequence 27774, A
c	31	58	34.3	787	8	US-11-266-748A-68635	Sequence 68635, A
c	32	58	34.3	787	8	US-11-266-748A-104963	Sequence 104963,
	33	58	34.3	787	8	US-11-266-748A-121446	Sequence 121446,
	34	58	34.3	1000	8	US-11-266-748A-221803	Sequence 221803,
	35	58	34.3	1000	8	US-11-266-748A-287165	Sequence 287165,
c	36	58	34.3	1000	8	US-11-266-748A-338594	Sequence 338594,
	37	58	34.3	1000	8	US-11-266-748A-397780	Sequence 397780,
c	38	58	34.3	1000	8	US-11-266-748A-468826	Sequence 468826,
	39	57	33.7	700	8	US-11-266-748A-480122	Sequence 480122,
	40	57	33.7	816	8	US-11-266-748A-354233	Sequence 354233,
	41	57	33.7	816	8	US-11-266-748A-384829	Sequence 384829,

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[start](#)

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:35:25 ; Search time 3516.55 Seconds
(without alignments)
787.138 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102055_128/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561@CGN_1_1_17145@runat_11082006_102055_128 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_hlc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
c	1	69	40.8	272	3	BQ391397	BQ391397 NISC_mq18
c	2	69	40.8	1039	14	DU940520	DU940520 367266 To
	3	69	40.8	1336	10	DV792849	DV792849 Hw-loin_3
	4	68.5	40.5	378	9	DN258017	DN258017 Meso07572
	5	68	40.2	424	2	BG897859	BG897859 HOA25-1-G
c	6	67.5	39.9	586	1	AV602344	AV602344 AV602344
	7	67	39.6	658	2	BF791971	BF791971 602252358
c	8	67	39.6	730	14	CT043835	CT043835 Sus scrof
	9	66	39.1	509	3	BP958426	BP958426 BP958426
	10	66	39.1	526	3	BU613702	BU613702 UI-M-EW0-
	11	66	39.1	590	4	BX478955	BX478955 DKFZp686C
c	12	66	39.1	644	8	CV276430	CV276430 WS0179.B2
	13	66	39.1	790	9	CX623722	CX623722 H11_A1 Sp
	14	65.5	38.8	760	14	CT396333	CT396333 Sus scrof
	15	65	38.5	374	7	BE235687	BE235687 143260 MA
	16	65	38.5	473	5	CF957818	CF957818 1694rsice
	17	64.5	38.2	227	1	AA877706	AA877706 nr09g06.s
c	18	64.5	38.2	510	1	AJ683647	AJ683647 AJ683647
c	19	64.5	38.2	510	2	BI680031	BI680031 457364 MA
c	20	64.5	38.2	592	4	BX915868	BX915868 BX915868
c	21	64.5	38.2	592	4	BX926799	BX926799 BX926799
c	22	64.5	38.2	636	3	BP165086	BP165086 BP165086
c	23	64.5	38.2	677	10	DV230344	DV230344 EST-AR167
c	24	64.5	38.2	687	8	CN004424	CN004424 ip46e03.g
c	25	64.5	38.2	697	10	DV224495	DV224495 EST-AR181
c	26	64.5	38.2	771	5	CJ018839	CJ018839 CJ018839
c	27	64.5	38.2	788	3	BP439064	BP439064 BP439064
c	28	64.5	38.2	833	4	BW971958	BW971958 BW971958
c	29	64.5	38.2	834	5	CJ029697	CJ029697 CJ029697
c	30	64.5	38.2	844	9	DN107178	DN107178 1104600 M
c	31	64.5	38.2	853	3	BP172960	BP172960 BP172960
c	32	64.5	38.2	859	4	BW979844	BW979844 BW979844
c	33	64.5	38.2	861	5	CJ023153	CJ023153 CJ023153
c	34	64.5	38.2	864	3	BP169610	BP169610 BP169610
c	35	64.5	38.2	868	4	BW976062	BW976062 BW976062
c	36	64	37.9	179	12	CC178380	CC178380 XD075 Bay
c	37	64	37.9	303	1	AV161371	AV161371 AV161371
	38	64	37.9	593	12	CE041369	CE041369 tigr-gss-

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This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-12.p2n.rge.

[start](#)

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:33:24 ; Search time 4111.77 Seconds
(without alignments)
886.481 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKALKKKALKKKALS YAVALSQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102053_91/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10617561@CGN_1_1_6362@runat_11082006_102053_91 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*

2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	87	47.3	539	2	AR079926	AR079926 Sequence
	2	87	47.3	539	2	AR178277	AR178277 Sequence
	3	87	47.3	539	2	AR478110	AR478110 Sequence
	4	84	45.7	468	5	HUMCGBBA3	K03183 Human chori
	5	84	45.7	475	5	HUMCGBEL03	K03189 Human chori
	6	84	45.7	498	5	BT006890	BT006890 Homo sapi
	7	84	45.7	498	8	AY889866	AY889866 Synthetic
	8	84	45.7	498	8	AY890611	AY890611 Synthetic
	9	84	45.7	498	8	AY892341	AY892341 Synthetic
	10	84	45.7	498	8	AY892342	AY892342 Synthetic
	11	84	45.7	498	8	AY893091	AY893091 Synthetic
	12	84	45.7	498	8	BT007573	BT007573 Synthetic
	13	84	45.7	516	5	BC069367	BC069367 Homo sapi
	14	84	45.7	519	5	BC106724	BC106724 Homo sapi
	15	84	45.7	520	5	BC106723	BC106723 Homo sapi
	16	84	45.7	524	5	BC069526	BC069526 Homo sapi
	17	84	45.7	530	2	BD078016	BD078016 Thyroid-s
	18	84	45.7	539	2	BD236914	BD236914 Chorionic
	19	84	45.7	539	2	AR345119	AR345119 Sequence
	20	84	45.7	539	2	AR360783	AR360783 Sequence
	21	84	45.7	539	2	AR399260	AR399260 Sequence
	22	84	45.7	539	2	AR481838	AR481838 Sequence
	23	84	45.7	539	2	AR590784	AR590784 Sequence
	24	84	45.7	539	5	HUMCGB	J00117 Human chori
c	25	84	45.7	549	2	AR154352	AR154352 Sequence
c	26	84	45.7	549	2	AR156976	AR156976 Sequence
c	27	84	45.7	549	2	BD140380	BD140380 Method fo
	28	84	45.7	555	2	CQ769367	CQ769367 Sequence
	29	84	45.7	575	2	AR154351	AR154351 Sequence
	30	84	45.7	575	2	AR156975	AR156975 Sequence
	31	84	45.7	575	2	BD140379	BD140379 Method fo
	32	84	45.7	587	2	AR257363	AR257363 Sequence
	33	84	45.7	607	5	BC103969	BC103969 Homo sapi
	34	84	45.7	607	5	BC103971	BC103971 Homo sapi
	35	84	45.7	611	5	BC103970	BC103970 Homo sapi
c	36	84	45.7	717	2	AR154332	AR154332 Sequence
c	37	84	45.7	717	2	AR154342	AR154342 Sequence

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[Score Home Page](#)
[Retrieve Application List](#)
[SCORE System Overview](#)
[SCORE FAQ](#)
[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-12.p2n.rng.

[start](#)

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:32:04 ; Search time 382.774 Seconds
(without alignments)
1038.259 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKALKKLKKALKKALSVAVALSCQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102051_79/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561@CGN_1_1_1975@runat_11082006_102051_79 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*

2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match Length	DB	ID	
	1	87	47.3	539	2	AAV04780 Human cho
	2	87	47.3	539	2	AAV18517 Human bet
	3	87	47.3	539	2	AAV04779 Human cho
c	4	84	45.7	332	12	ACH88458 Human gen
	5	84	45.7	498	12	ADN49743 Beta subu
	6	84	45.7	498	13	ADU74419 Human cho
	7	84	45.7	498	14	AED73859 Human pla
	8	84	45.7	534	3	Aaz90609 Human bet
	9	84	45.7	539	2	Aax25387 Human cho
	10	84	45.7	539	3	AAA73833 Human cho
	11	84	45.7	539	11	ADM64531 Beta-huma
	12	84	45.7	539	12	ADH52593 Human cho
	13	84	45.7	539	12	ADH52556 Human cho
	14	84	45.7	539	12	ADK39744 DNA encod
	15	84	45.7	539	13	ADT90936 Human bet
	16	84	45.7	543	6	ADE50947 hCG-LH fu
c	17	84	45.7	549	4	AAD08808 Human sin
c	18	84	45.7	554	12	ACH74758 Human gen
	19	84	45.7	555	10	ADI62650 Human apo
	20	84	45.7	575	2	AAT03240 Human CG
	21	84	45.7	575	4	AAS08507 DNA encod
	22	84	45.7	575	4	AAD08807 Human sin
	23	84	45.7	579	2	AAQ14800 Human cho
	24	84	45.7	587	2	Aaz31734 Human cho
c	25	84	45.7	717	4	AAD08788 Human sin
c	26	84	45.7	717	4	AAD08800 Human sin
c	27	84	45.7	717	4	AAD08798 Human sin
	28	84	45.7	725	2	Aaz31742 Human CG
	29	84	45.7	725	2	Aaz31751 Human CG
	30	84	45.7	725	2	Aaz31750 Human CG
c	31	84	45.7	726	4	AAD08796 Human sin
	32	84	45.7	732	13	ADQ83691 Human tum
	33	84	45.7	732	13	ADQ83690 Human tum
	34	84	45.7	743	2	AAT03233 Single ch
	35	84	45.7	743	2	AAT03231 Single ch
	36	84	45.7	743	2	AAT03219 Single ch
	37	84	45.7	743	4	AAS08499 DNA encod

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This page gives you Search Results detail for the Application 10617561 and Search Result us-10-6: 12.p2n.rni.

[start](#)

[Go Back to previc](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:51:34 ; Search time 120.102 Seconds
(without alignments)
888.020 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKALKKKLKKALKKALS YAVALSQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102057_179/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10617561_@CGN_1_1_529_@runat_11082006_102057_179 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

```

3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	87	47.3	539	2	US-08-709-924-1	Sequence 1, Appli
2	87	47.3	539	2	US-08-709-925-1	Sequence 1, Appli
3	87	47.3	539	3	US-08-709-948-1	Sequence 1, Appli
4	87	47.3	539	3	US-10-050-875-1	Sequence 1, Appli
5	84	45.7	539	3	US-09-220-415-1	Sequence 1, Appli
6	84	45.7	539	3	US-09-675-776-1	Sequence 1, Appli
7	84	45.7	539	3	US-09-676-739-1	Sequence 1, Appli
8	84	45.7	539	3	US-09-675-362-1	Sequence 1, Appli
9	84	45.7	539	3	US-09-677-152-1	Sequence 1, Appli
c 10	84	45.7	549	3	US-08-918-288-37	Sequence 37, Appl
c 11	84	45.7	549	3	US-09-282-357-37	Sequence 37, Appl
12	84	45.7	575	3	US-08-918-288-35	Sequence 35, Appl
13	84	45.7	575	3	US-09-282-357-35	Sequence 35, Appl
14	84	45.7	575	5	US-08-867-587B-35	Sequence 35, Appl
15	84	45.7	587	3	US-09-059-625-2	Sequence 2, Appli
c 16	84	45.7	717	3	US-08-918-288-7	Sequence 7, Appli
c 17	84	45.7	717	3	US-08-918-288-22	Sequence 22, Appl
c 18	84	45.7	717	3	US-08-918-288-25	Sequence 25, Appl
c 19	84	45.7	717	3	US-09-282-357-7	Sequence 7, Appli
c 20	84	45.7	717	3	US-09-282-357-22	Sequence 22, Appl
c 21	84	45.7	717	3	US-09-282-357-25	Sequence 25, Appl
22	84	45.7	725	3	US-09-059-625-36	Sequence 36, Appl
23	84	45.7	725	3	US-09-059-625-50	Sequence 50, Appl
24	84	45.7	725	3	US-09-059-625-55	Sequence 55, Appl
c 25	84	45.7	726	3	US-08-918-288-19	Sequence 19, Appl
c 26	84	45.7	726	3	US-09-282-357-19	Sequence 19, Appl
27	84	45.7	743	3	US-08-918-288-5	Sequence 5, Appli
28	84	45.7	743	3	US-08-918-288-20	Sequence 20, Appl
29	84	45.7	743	3	US-08-918-288-23	Sequence 23, Appl
30	84	45.7	743	3	US-09-282-357-5	Sequence 5, Appli
31	84	45.7	743	3	US-09-282-357-20	Sequence 20, Appl
32	84	45.7	743	3	US-09-282-357-23	Sequence 23, Appl
33	84	45.7	743	5	US-08-867-587B-5	Sequence 5, Appli
34	84	45.7	743	5	US-08-867-587B-20	Sequence 20, Appl
35	84	45.7	743	5	US-08-867-587B-23	Sequence 23, Appl
36	84	45.7	752	3	US-08-918-288-17	Sequence 17, Appl
37	84	45.7	752	3	US-09-282-357-17	Sequence 17, Appl
38	84	45.7	752	5	US-08-867-587B-17	Sequence 17, Appl
c 39	84	45.7	834	3	US-08-918-288-4	Sequence 4, Appli
c 40	84	45.7	834	3	US-09-282-357-4	Sequence 4, Appli
c 41	84	45.7	835	3	US-08-918-288-40	Sequence 40, Appl
c 42	84	45.7	835	3	US-09-282-357-40	Sequence 40, Appl
43	84	45.7	836	3	US-08-918-288-2	Sequence 2, Appli

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-12.p2n.rnpbm.

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This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-12.p2n.rnpbm.

[start](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:58:24 ; Search time 1273.42 Seconds
(without alignments)
550.013 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKKALKKKALKKKALSYAVALSCQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102100_235/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10617561@CGN_1_1_5513@runat_11082006_102100_235 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

```

2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
<hr/>							
c	1	87	47.3	539	6	US-10-050-875-1	Sequence 1, Appli
	2	84	45.7	332	7	US-10-029-386-21653	Sequence 21653, A
	3	84	45.7	495	16	US-11-235-621-4	Sequence 4, Appli
	4	84	45.7	498	8	US-10-411-037-71	Sequence 71, Appl
	5	84	45.7	498	8	US-10-411-026-71	Sequence 71, Appl
	6	84	45.7	498	8	US-10-410-962-71	Sequence 71, Appl
	7	84	45.7	498	8	US-10-411-049-71	Sequence 71, Appl
	8	84	45.7	498	8	US-10-410-930-71	Sequence 71, Appl
	9	84	45.7	498	8	US-10-410-997-71	Sequence 71, Appl
	10	84	45.7	498	8	US-10-411-012-71	Sequence 71, Appl
	11	84	45.7	498	8	US-10-410-913-71	Sequence 71, Appl
	12	84	45.7	498	9	US-10-410-980-71	Sequence 71, Appl
	13	84	45.7	498	10	US-10-410-897-71	Sequence 71, Appl
	14	84	45.7	498	10	US-10-821-234-687	Sequence 687, App
	15	84	45.7	530	9	US-10-788-383-3	Sequence 3, Appli
	16	84	45.7	539	3	US-09-466-320-15	Sequence 15, Appl
	c 17	84	45.7	554	7	US-10-029-386-7953	Sequence 7953, Ap
	18	84	45.7	879	16	US-11-219-339-3	Sequence 3, Appli
	19	84	45.7	880	8	US-10-734-564-57	Sequence 57, Appl
	20	84	45.7	893	3	US-09-760-294-3	Sequence 3, Appli
	21	84	45.7	893	3	US-09-760-294-5	Sequence 5, Appli
	22	84	45.7	893	3	US-09-760-294-6	Sequence 6, Appli
	23	84	45.7	893	3	US-09-760-294-7	Sequence 7, Appli
	24	84	45.7	893	3	US-09-760-294-8	Sequence 8, Appli
	25	84	45.7	893	3	US-09-760-294-9	Sequence 9, Appli
	26	84	45.7	893	3	US-09-760-294-10	Sequence 10, Appl
	c 27	84	45.7	998	12	US-10-301-480-583005	Sequence 583005,
	c 28	84	45.7	998	12	US-10-301-480-1196414	Sequence 1196414,
	29	84	45.7	1202	3	US-09-756-186-3	Sequence 3, Appli
	30	84	45.7	1202	9	US-10-724-226-3	Sequence 3, Appli
	31	84	45.7	1301	3	US-09-756-186-7	Sequence 7, Appli
	32	84	45.7	1301	9	US-10-724-226-7	Sequence 7, Appli
	33	84	45.7	1325	9	US-10-769-144-11	Sequence 11, Appl
	34	84	45.7	1325	10	US-10-903-191-11	Sequence 11, Appl
	35	84	45.7	1542	16	US-11-235-621-18	Sequence 18, Appl
	36	84	45.7	1842	9	US-10-769-144-9	Sequence 9, Appli

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[start](#)

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:35:25 ; Search time 4049.36 Seconds
(without alignments)
787.138 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKALKKLKKALKKALS YAVALSQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102055_128/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561@CGN_1_1_17145@runat_11082006_102055_128 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match Length	DB	ID		
c	1	92	50.0	255	10	R63352	R63352 yi07h10.s1
	2	90	48.9	378	7	BF369834	BF369834 QV4-GN012
	3	88	47.8	905	3	BM810215	BM810215 AGENCOURT
c	4	87	47.3	248	10	H95381	H95381 yw60d07.s1
c	5	87	47.3	254	3	BU752621	BU752621 UI-1-BC0-
c	6	87	47.3	367	10	H94446	H94446 yw55f02.s1
c	7	87	47.3	473	1	AA400910	AA400910 zt71h09.s
c	8	87	47.3	473	10	N27302	N27302 yw71f12.s1
c	9	87	47.3	515	10	N30608	N30608 yw72c07.s1
c	10	87	47.3	526	1	AA644163	AA644163 af62d08.s
c	11	87	47.3	531	10	W71989	W71989 zd66b03.s1
c	12	87	47.3	548	10	N30036	N30036 yw80b11.s1
c	13	87	47.3	564	10	N32604	N32604 yw95d03.s1
c	14	87	47.3	593	10	N29730	N29730 yw78h03.s1
c	15	87	47.3	601	10	N32759	N32759 yw91b05.s1
	16	85	46.2	867	4	BX379814	BX379814 BX379814
	17	85	46.2	1108	3	BM909276	BM909276 AGENCOURT
	18	84	45.7	251	1	AA330413	AA330413 EST34462
c	19	84	45.7	255	5	CF527786	CF527786 UI-1-BC0-
c	20	84	45.7	258	5	CF527734	CF527734 UI-1-BC0-
c	21	84	45.7	260	3	BU752347	BU752347 UI-1-BC0-
c	22	84	45.7	266	10	H93668	H93668 yw55c12.s1
c	23	84	45.7	279	5	CF527738	CF527738 UI-1-BC0-
c	24	84	45.7	279	5	CF528202	CF528202 UI-1-BC0-
c	25	84	45.7	280	5	CF527893	CF527893 UI-1-BC0-
c	26	84	45.7	284	10	H93656	H93656 yw55a11.s1
c	27	84	45.7	291	3	BQ003972	BQ003972 UI-1-BC0-
c	28	84	45.7	299	5	CF527823	CF527823 UI-1-BC0-
c	29	84	45.7	299	5	CF528125	CF528125 UI-1-BC0-
c	30	84	45.7	305	3	BU752444	BU752444 UI-1-BC0-
c	31	84	45.7	308	5	CF528150	CF528150 UI-1-BC0-
c	32	84	45.7	309	3	BQ007333	BQ007333 UI-1-BC0-
c	33	84	45.7	309	5	CF528240	CF528240 UI-1-BC0-
c	34	84	45.7	313	3	BQ004094	BQ004094 UI-1-BC0-
c	35	84	45.7	313	3	BQ007393	BQ007393 UI-1-BC0-
c	36	84	45.7	313	3	BU752304	BU752304 UI-1-BC0-
c	37	84	45.7	313	3	BU752610	BU752610 UI-1-BC0-
c	38	84	45.7	313	5	CF527771	CF527771 UI-1-BC0-

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-15.p2n.rge.

[Score Home Page](#)
[Retrieve Application List](#)
[SCORE System Overview](#)
[SCORE FAQ](#)
[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-15.p2n.rge.

[start](#)

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:33:24 ; Search time 3570.74 Seconds
(without alignments)
886.481 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKALKKKLKKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102053_91/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10617561@CGN_1_1_6362@runat_11082006_102053_91 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*

2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	82	48.5	710	11	AY307177	AY307177 Lampetra
	2	80	47.3	722	11	AY307176	AY307176 Lampetra
	3	80	47.3	723	11	AY307175	AY307175 Ichthyomy
	4	80	47.3	728	11	AY307174	AY307174 Ichthyomy
	5	80	47.3	732	11	AY307178	AY307178 Lampetra
	6	80	47.3	750	2	AR778646	AR778646 Sequence
	7	76	45.0	718	2	AR778647	AR778647 Sequence
	8	76	45.0	718	11	AY052628	AY052628 Petromyzo
	9	75	44.4	774	11	AY307172	AY307172 Geotria a
	10	75	44.4	790	2	AR778644	AR778644 Sequence
	11	72	42.6	666	11	AY307173	AY307173 Mordacia
c	12	70	41.4	183117	12	AC097012	AC097012 Sus scrof
	13	70	41.4	191474	5	AC018450	AC018450 Homo sapi
	14	69	40.8	676	2	AR778645	AR778645 Sequence
c	15	69	40.8	175569	6	AC102282	AC102282 Mus muscu
c	16	69	40.8	223318	12	AC095389	AC095389 Rattus no
c	17	69	40.8	269719	12	AC136277	AC136277 Rattus no
c	18	68	40.2	263287	12	AC171986	AC171986 Bos tauru
c	19	67	39.6	110000	15	AE010299_21	Continuation (22 o
	20	66.5	39.3	110000	15	AE016877_47	Continuation (48 o
c	21	66	39.1	29963	5	AL356859	AL356859 Human DNA
	22	66	39.1	167388	12	AC157445	AC157445 Sus scrof
c	23	66	39.1	168091	6	AC139553	AC139553 Mus muscu
	24	66	39.1	182733	6	AC123941	AC123941 Mus muscu
c	25	64.5	38.2	1618	14	SSC293581	AJ293581 Sus scrof
c	26	64.5	38.2	1730	2	I33464	I33464 Sequence 1
c	27	64.5	38.2	1730	2	I36536	I36536 Sequence 1
c	28	64.5	38.2	1730	2	I58393	I58393 Sequence 1
	29	64.5	38.2	185146	12	AC175181	AC175181 Bos tauru
	30	64	37.9	2468	5	BC053878	BC053878 Homo sapi
	31	64	37.9	60563	12	AC137682	AC137682 Homo sapi
	32	64	37.9	65002	12	AC136362	AC136362 Homo sapi
	33	64	37.9	110000	12	CR931980_2	Continuation (3 of
c	34	64	37.9	158892	12	AC132819	AC132819 Homo sapi
c	35	64	37.9	163681	5	AL136992	AL136992 Human DNA
c	36	64	37.9	188340	5	AC135178	AC135178 Homo sapi
	37	64	37.9	204939	12	AC156047	AC156047 Bos tauru